

Rec'd PCT/PTO 01 MAR 2006

10/537612

**RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/537,612  
Source: PCF  
Date Processed by STIC: 3/1/06

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PCT

## RAW SEQUENCE LISTING

DATE: 03/01/2006

PATENT APPLICATION: US/10/537,612

TIME: 13:55:57

Input Set : A:\Q88296 - 10-537,612 sequence listing.txt

Output Set: N:\CRF4\03012006\J537612.raw

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3 <110> APPLICANT: Imperial College Innovations Ltd
5 <120> TITLE OF INVENTION: Engineering Redox Proteins
7 <130> FILE REFERENCE: Q88296
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/537,612
C--> 10 <141> CURRENT FILING DATE: 2005-06-03
12 <160> NUMBER OF SEQ ID NOS: 11
14 <170> SOFTWARE: PatentIn Ver. 2.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 84
18 <212> TYPE: DNA
19 <213> ORGANISM: Escherichia coli
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)..(84)
24 <223> OTHER INFORMATION: Helix 1 of E.coli repressor of primer (rop)
26 <400> SEQUENCE: 1
27 acc aaa caa gaa aaa acc gcc ctt aac atg gcc cgc ttt atc aga agc   48
28 Thr Lys Gln Glu Lys Thr Ala Leu Asn Met Ala Arg Phe Ile Arg Ser
29   1           5           10           15
31 cag aca tta acg ctt ctg gag aaa ctc aac gag ctg   84
32 Gln Thr Leu Thr Leu Leu Glu Lys Leu Asn Glu Leu
33   20           25
36 <210> SEQ ID NO: 2
37 <211> LENGTH: 28
38 <212> TYPE: PRT
39 <213> ORGANISM: Escherichia coli
41 <400> SEQUENCE: 2
42 Thr Lys Gln Glu Lys Thr Ala Leu Asn Met Ala Arg Phe Ile Arg Ser
43   1           5           10           15
45 Gln Thr Leu Thr Leu Leu Glu Lys Leu Asn Glu Leu
46   20           25
50 <210> SEQ ID NO: 3
51 <211> LENGTH: 84
52 <212> TYPE: DNA
53 <213> ORGANISM: Escherichia coli
55 <220> FEATURE:
56 <221> NAME/KEY: CDS
57 <222> LOCATION: (1)..(84)
58 <223> OTHER INFORMATION: Helix 2 of rop
60 <400> SEQUENCE: 3
61 gat gaa cag gca gac atc tgt gaa tcg ctt cac gac cac gct gat gag   48
62 Asp Glu Gln Ala Asp Ile Cys Glu Ser Leu His Asp His Ala Asp Glu
63   1           5           10           15

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65 ctt tac cgc agc tgc ctt gcc cgt ttc ggc gac gac      84
66 Leu Tyr Arg Ser Cys Leu Ala Arg Phe Gly Asp Asp
67          20          25
70 <210> SEQ ID NO: 4
71 <211> LENGTH: 28
72 <212> TYPE: PRT
73 <213> ORGANISM: Escherichia coli
75 <400> SEQUENCE: 4
76 Asp Glu Gln Ala Asp Ile Cys Glu Ser Leu His Asp His Ala Asp Glu
77  1          5          10          15
79 Leu Tyr Arg Ser Cys Leu Ala Arg Phe Gly Asp Asp
80          20          25
84 <210> SEQ ID NO: 5
85 <211> LENGTH: 192
86 <212> TYPE: DNA
87 <213> ORGANISM: Escherichia coli
89 <220> FEATURE:
90 <221> NAME/KEY: CDS
91 <222> LOCATION: (1)..(192)
92 <223> OTHER INFORMATION: wild type dimeric rop
94 <400> SEQUENCE: 5
95 atg ggt acc aaa caa gaa aaa acc gcc ctt aac atg gcc cgc ttt atc      48
96 Met Gly Thr Lys Gln Glu Lys Thr Ala Leu Asn Met Ala Arg Phe Ile
97  1          5          10          15
99 aga agc cag aca tta acg ctt ctg gag aaa ctc aac gag ctg gac gcg      96
100 Arg Ser Gln Thr Leu Thr Leu Leu Glu Lys Leu Asn Glu Leu Asp Ala
101          20          25          30
103 gat gaa cag gca gac atc tgt gaa tcg ctt cac gac cac gct gat gag      144
104 Asp Glu Gln Ala Asp Ile Cys Glu Ser Leu His Asp His Ala Asp Glu
105          35          40          45
107 ctt tac cgc agc tgc ctt gcc cgt ttc ggc gac gac ggt gaa aac ctg      192
108 Leu Tyr Arg Ser Cys Leu Ala Arg Phe Gly Asp Asp Gly Glu Asn Leu
109          50          55          60
112 <210> SEQ ID NO: 6
113 <211> LENGTH: 64
114 <212> TYPE: PRT
115 <213> ORGANISM: Escherichia coli
117 <400> SEQUENCE: 6
118 Met Gly Thr Lys Gln Glu Lys Thr Ala Leu Asn Met Ala Arg Phe Ile
119  1          5          10          15
121 Arg Ser Gln Thr Leu Thr Leu Leu Glu Lys Leu Asn Glu Leu Asp Ala
122          20          25          30
124 Asp Glu Gln Ala Asp Ile Cys Glu Ser Leu His Asp His Ala Asp Glu
125          35          40          45
127 Leu Tyr Arg Ser Cys Leu Ala Arg Phe Gly Asp Asp Gly Glu Asn Leu
128          50          55          60
132 <210> SEQ ID NO: 7
133 <211> LENGTH: 384
134 <212> TYPE: DNA

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135 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
138 <223> OTHER INFORMATION: Description of Artificial Sequence: Monomeric rop
139     containing all 4 helices in one continuous
140     sequence
142 <220> FEATURE:
143 <221> NAME/KEY: CDS
144 <222> LOCATION: (1)..(384)
145 <223> OTHER INFORMATION: Monomeric rop consisting of helices 1-1'-2'-2 and
146     helices 1 and 1', and 2' and 2 are connected by
147     GGGGG loops
149 <400> SEQUENCE: 7
150 atg ggt acc aaa caa gaa aaa acc gcc ctt aac atg gcc cgc ttt atc      48
151 Met Gly Thr Lys Gln Glu Lys Thr Ala Leu Asn Met Ala Arg Phe Ile
152   1             5             10             15
154 aga agc cag aca tta acg ctt ctg gag aaa ctc aac gag ctg ggt ggc      96
155 Arg Ser Gln Thr Leu Thr Leu Leu Glu Lys Leu Asn Glu Leu Gly Gly
156   20             25             30
158 ggt ggc ggt acc aac caa gag aag acc gcc ctt aac atg gcc cgc ttt      144
159 Gly Gly Gly Thr Lys Gln Glu Lys Thr Ala Leu Asn Met Ala Arg Phe
160   35             40             45
162 atc aga tct cag aca tta acg ctt cta gag aag ctt aac gag ctc ggg      192
163 Ile Arg Ser Gln Thr Leu Thr Leu Leu Glu Lys Leu Asn Glu Leu Gly
164   50             55             60
166 gcg gat gaa cag gca gac ata tgt gaa tcg ctt cac gac cac gct gat      240
167 Ala Asp Glu Gln Ala Asp Ile Cys Glu Ser Leu His Asp His Ala Asp
168   65             70             75             80
170 gag ctt tac cgc agc tgc ctt gcc cgt ttc ggt ggc ggt ggc ggt gcg      288
171 Glu Leu Tyr Arg Ser Cys Leu Ala Arg Phe Gly Gly Gly Gly Gly Ala
172   85             90             95
174 gat gaa cag gca gac atc tgt gaa tcg ctt cac gac cac gct gat gag      336
175 Asp Glu Gln Ala Asp Ile Cys Glu Ser Leu His Asp His Ala Asp Glu
176   100            105            110
178 ctt tac cgc agc tgc ctt gcc cgt ttc ggc gac gac ggt gaa aac ctg      384
179 Leu Tyr Arg Ser Cys Leu Ala Arg Phe Gly Asp Asp Gly Glu Asn Leu
180   115            120            125
183 <210> SEQ ID NO: 8
184 <211> LENGTH: 128
185 <212> TYPE: PRT
186 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
189 <223> OTHER INFORMATION: Description of Artificial Sequence: Monomeric rop
190     containing all 4 helices in one continuous
191     sequence
193 <400> SEQUENCE: 8
194 Met Gly Thr Lys Gln Glu Lys Thr Ala Leu Asn Met Ala Arg Phe Ile
195   1             5             10             15
197 Arg Ser Gln Thr Leu Thr Leu Leu Glu Lys Leu Asn Glu Leu Gly Gly
198   20             25             30

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200 Gly Gly Gly Thr Lys Gln Glu Lys Thr Ala Leu Asn Met Ala Arg Phe
201      35              40              45
203 Ile Arg Ser Gln Thr Leu Thr Leu Leu Glu Lys Leu Asn Glu Leu Gly
204      50              55              60
206 Ala Asp Glu Gln Ala Asp Ile Cys Glu Ser Leu His Asp His Ala Asp
207 65              70              75              80
209 Glu Leu Tyr Arg Ser Cys Leu Ala Arg Phe Gly Gly Gly Gly Gly Ala
210              85              90              95
212 Asp Glu Gln Ala Asp Ile Cys Glu Ser Leu His Asp His Ala Asp Glu
213      100              105              110
215 Leu Tyr Arg Ser Cys Leu Ala Arg Phe Gly Asp Asp Gly Glu Asn Leu
216      115              120              125
220 <210> SEQ ID NO: 9
221 <211> LENGTH: 19
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Description of Artificial Sequence: psp7 upstream
227      amplification sequence
229 <400> SEQUENCE: 9
230 gcgaaattaa tacgactca
233 <210> SEQ ID NO: 10
234 <211> LENGTH: 23
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION: Description of Artificial Sequence: asp4
240      downstream amplification sequence
242 <400> SEQUENCE: 10
243 gttggctgct gccaccgctg agc
246 <210> SEQ ID NO: 11
247 <211> LENGTH: 128
248 <212> TYPE: PRT
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: Description of Artificial Sequence: RDM14.5
254 <400> SEQUENCE: 11
255 Met Gly Thr Lys Gln Glu Lys Thr Ala Leu Asn Met Ala Arg Phe Ile
256 1              5              10              15
258 Arg Ser Gln Thr Leu Thr Leu Leu Glu Lys Leu Asn Glu Leu Gly Gly
259      20              25              30
261 Gly Gly Gly Thr Lys Gln Glu Lys Thr Ala Leu Asn Met Ala Arg Phe
262      35              40              45
264 Ile Arg Ser Gln Thr Leu Thr His Leu Glu Lys Leu Asn Glu Leu Gly
265      50              55              60
267 Ala Asp Glu Gln Ala Asp Ile Cys Glu Ser Leu Ala Asp Trp Ala Asp
268 65              70              75              80
270 Glu Leu Tyr Arg Ser Cys Leu Ala Arg Phe Gly Gly Gly Gly Gly Ala
271      85              90              95

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273	Asp	Glu	Gln	Ala	Asp	Ile	Cys	Glu	Ser	Leu	Ala	Asp	Trp	Ala	Asp	Glu
274				100					105					110		
276	His	Tyr	Arg	Ser	Cys	Leu	Ala	Arg	Phe	Gly	Asp	Asp	Gly	Glu	Asn	Leu
277				115				120					125			

**VERIFICATION SUMMARY**

DATE: 03/01/2006

PATENT APPLICATION: US/10/537,612

TIME: 13:55:58

Input Set : A:\Q88296 - 10-537,612 sequence listing.txt

Output Set: N:\CRF4\03012006\J537612.raw

L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date